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<110> Hermon-Taylor, John  
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<120> NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES IN PATHOGENIC  
 MYCOBACTERIA AND THEIR USE AS DIAGNOSTICS, VACCINES AND  
 TARGETS FOR CHEMOTHERAPY

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<140> 09/091,538

<141> 1998-06-19

<150> PCT/GB96/03221

<151> 1996-12-23

<150> GB 9526178.0

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 ggatttacgg atccgcgcaa tggtcgaatg cttcaagctg acggcatttt cttccgtggg 3180  
 gacgattgac ataaatgctt gcgtcggcac cctgccggta tccaaacggg cgatctggtg 3240  
 agccggcctc ccgggcacct aatcgactat ctaaattgag gcggccgcga cgtgcggcac 3300  
 gaacaggtgg ccggctgcta gcgttacaca cgatcatgact gcgccagtgt tctcgataat 3360  
 tatccctacc ttcaatgcag cggtagcgt gcaagcctgc ctcggaagca tcgtcgggca 3420  
 gacctaccgg gaagtggaa tggtccttgt cgacggcggt tcgaccgatc ggacctcga 3480  
 catcggaac agtttccgcc cggaactcgg ctccgcactg gtcgttcaca gggggccga 3540



tgatggcccc tacgacgcca tgaaccgcgg cgctggcgta gccacaggcg aatgggtact 3600  
 ttttttaggc gccgacgaca cctctacga accaaccacg ttggcccagg tagccgcttt 3660  
 tctcggcgac catgcggcaa gccatcttgt ctatggcgat gttgtgatgc gttcgacgaa 3720  
 aagccggcat gccggacctt tcgacctcga ccgcctccta tttgagacga atttgtgcc 3780  
 ccaatcgatc ttttaccgcc gtgagctttt cgacggcatc ggcccttaca acctgcgcta 3840  
 ccgagtctgg gcggactggg acttcaatat tcgctgcttc tccaaccgg cgctgattac 3900  
 ccgctacatg gacgtcgtga tttccgaata caacgacatg accggcttca gcatgaggca 3960  
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 gacttgacgg cgcatgctgg cgtttttgaa agacaaggag aatcgccgtc tggccttgcg 4080  
 tacgcggttg ataagggtta aggccgtctc caaagaacga agcgcagaac cgtagtcgcg 4140  
 gatccacatt ggacttcttt aacgcgtttg cgtcctgac cacttttcaa ccccgttccg 4200  
 cgtgacgcgg cgcgacgaga gtggtcgcat atcgcgtcac tgttctcgtg ccagtgcctg 4260  
 gaaagcgctg agcactctgg ttgcggttct tgacgttcgc gcccgcccct agaggtagcg 4320  
 tgtcacgtga ctgaagccaa tgagtccaac tcggcgctgc gaaaggtttc agtcgcggtt 4380  
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 tcg acg atc acc ttg tac cgg tcg atg tat gac cca atg tcg tcc gca 96  
 Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala  
 20 25 30  
 acc gag aag acg tac gtc agg tcc gcc gcc ccg ctt tca ccc atg ggc 144  
 Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly  
 35 40 45  
 gtc ggg acg gcg atg aaa atg acg tcc gcg tgc tcg att ccg cgt tgc 192  
 Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys  
 50 55 60  
 cgg tcg gtg gtg aag tca atc agc ccg ttc tca cgg ttc ctc gca atc 240  
 Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile  
 65 70 75 80

aac tcc caa ccc ggg ctc gaa aat cgg gac act gcc tgc gag gag caa 288  
 Asn Ser Gln Pro Gly Leu Glu Asn Arg Asp Thr Ala Cys Glu Glu Gln  
                     85                    90                    95

atc gat ctt ggc ctg atc gat atc gac aca gac gac atc gtt gcc gct 336  
 Ile Asp Leu Gly Leu Ile Asp Ile Asp Thr Asp Asp Ile Val Ala Ala  
                     100                    105                    110

atc cgc gag aca ggc gcc cgt gac gag gcc tac ata gcc tga 378  
 Ile Arg Glu Thr Gly Ala Arg Asp Glu Ala Tyr Ile Ala  
                     115                    120                    125

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 <212> PRT  
 <213> Mycobacterium

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Ser Thr Ile Thr Leu Tyr Arg Ser Met Tyr Asp Pro Met Ser Ser Ala  
                     20                    25                    30

Thr Glu Lys Thr Tyr Val Arg Ser Ala Ala Pro Leu Ser Pro Met Gly  
                     35                    40                    45

Val Gly Thr Ala Met Lys Met Thr Ser Ala Cys Ser Ile Pro Arg Cys  
                     50                    55                    60

Arg Ser Val Val Lys Ser Ile Ser Pro Phe Ser Arg Phe Leu Ala Ile  
                     65                    70                    75                    80

Asn Ser Gln Pro Gly Leu Glu Asn Arg Asp Thr Ala Cys Glu Glu Gln  
                     85                    90                    95

Ile Asp Leu Gly Leu Ile Asp Ile Asp Thr Asp Asp Ile Val Ala Ala  
                     100                    105                    110

Ile Arg Glu Thr Gly Ala Arg Asp Glu Ala Tyr Ile Ala  
                     115                    120                    125

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 <211> 834  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(831)

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           1                    5                    10                    15

ctc gag gga ttg aaa agc acc gtg gag agc gtt cgc gcg cag cgc tat	96
Leu Glu Gly Leu Lys Ser Thr Val Glu Ser Val Arg Ala Gln Arg Tyr	
20 25 30	
ggg ggg cga atc gag cac atc gtc atc gac ggt gga tcg ggc gac gcc	144
Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala	
35 40 45	
gtc gtg gag tat ctg tcc ggc gat cct ggc ttt gca tat tgg caa tct	192
Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser	
50 55 60	
cag ccc gac aac ggg aga tat gac gcg atg aat cag ggc att gcc cat	240
Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His	
65 70 75 80	
tcg tcg ggc gac ctg ttg tgg ttt atg cac tcc acg gat cgt ttc tcc	288
Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser	
85 90 95	
gat cca gat gca gtc gct tcc gtg gtg gag gcg ctc tcg ggg cat gga	336
Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly	
100 105 110	
cca gta cgt gat ttg tgg ggt tac ggg aaa aac aac ctt gtc gga ctc	384
Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu	
115 120 125	
gac ggc aaa cca ctt ttc cct cgg ccg tac ggc tat atg ccg ttt aag	432
Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys	
130 135 140	
atg cgg aaa ttt ctg ctc ggc gcg acg gtt gcg cat cag gcg aca ttc	480
Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe	
145 150 155 160	
ttc ggc gcg tcg ctg gta gcc aag ttg ggc ggt tac gat ctt gat ttt	528
Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe	
165 170 175	
gga ctc gag gcg gac cag ctg ttc atc tac cgt gcc gca cta ata cgg	576
Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg	
180 185 190	
cct ccc gtc acg atc gac cgc gtg gtt tgc gac ttc gat gtc acg gga	624
Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly	
195 200 205	
cct ggt tca acc cag ccc atc cgt gag cac tat cgg acc ctg cgg cgg	672
Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg	
210 215 220	
ctc tgg gac ctg cat ggc gac tac ccg ctg ggt ggg cgc aga gtg tcg	720
Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser	
225 230 235 240	
tgg gct tac ttg cgt gtg aag gag tac ttg att cgg gcc gac ctg gcc	768
Trp Ala Tyr Leu Arg Val Lys Glu Tyr Leu Ile Arg Ala Asp Leu Ala	
245 250 255	

gca ttc aac gcg gta aag ttc ttg cga gcg aag ttc gcc aga gct tcg 816  
 Ala Phe Asn Ala Val Lys Phe Leu Arg Ala Lys Phe Ala Arg Ala Ser  
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cgg aag caa aat tca tag 834  
 Arg Lys Gln Asn Ser  
                   275

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 <211> 277  
 <212> PRT  
 <213> Mycobacterium

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 Leu Glu Gly Leu Lys Ser Thr Val Glu Ser Val Arg Ala Gln Arg Tyr  
                   20                  25                  30  
 Gly Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Ala  
                   35                  40                  45  
 Val Val Glu Tyr Leu Ser Gly Asp Pro Gly Phe Ala Tyr Trp Gln Ser  
   50                  55                  60  
 Gln Pro Asp Asn Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala His  
   65                  70                  75                  80  
 Ser Ser Gly Asp Leu Leu Trp Phe Met His Ser Thr Asp Arg Phe Ser  
                   85                  90                  95  
 Asp Pro Asp Ala Val Ala Ser Val Val Glu Ala Leu Ser Gly His Gly  
                   100                  105                  110  
 Pro Val Arg Asp Leu Trp Gly Tyr Gly Lys Asn Asn Leu Val Gly Leu  
                   115                  120                  125  
 Asp Gly Lys Pro Leu Phe Pro Arg Pro Tyr Gly Tyr Met Pro Phe Lys  
   130                  135                  140  
 Met Arg Lys Phe Leu Leu Gly Ala Thr Val Ala His Gln Ala Thr Phe  
   145                  150                  155                  160  
 Phe Gly Ala Ser Leu Val Ala Lys Leu Gly Gly Tyr Asp Leu Asp Phe  
                   165                  170                  175  
 Gly Leu Glu Ala Asp Gln Leu Phe Ile Tyr Arg Ala Ala Leu Ile Arg  
                   180                  185                  190  
 Pro Pro Val Thr Ile Asp Arg Val Val Cys Asp Phe Asp Val Thr Gly  
                   195                  200                  205  
 Pro Gly Ser Thr Gln Pro Ile Arg Glu His Tyr Arg Thr Leu Arg Arg  
   210                  215                  220  
 Leu Trp Asp Leu His Gly Asp Tyr Pro Leu Gly Gly Arg Arg Val Ser  
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<222> (1)..(1029)
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Val	Lys	Arg	Ala	Leu	Ile	Thr	Gly	Ile	Thr	Gly	Gln	Asp	Gly	Ser	Tyr		
1				5					10					15			
ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt																	96
Leu	Ala	Glu	Leu	Leu	Leu	Ser	Lys	Gly	Tyr	Glu	Val	His	Gly	Leu	Val		
			20					25					30				
cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt																	144
Arg	Arg	Ala	Ser	Thr	Phe	Asn	Thr	Ser	Arg	Ile	Asp	His	Leu	Tyr	Val		
		35					40				45						
gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc																	192
Asp	Pro	His	Gln	Pro	Gly	Ala	Arg	Leu	Phe	Leu	His	Tyr	Ala	Asp	Leu		
	50					55					60						
act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat																	240
Thr	Asp	Gly	Thr	Arg	Leu	Val	Thr	Leu	Leu	Ser	Ser	Ile	Asp	Pro	Asp		
65					70				75					80			
gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac																	288
Glu	Val	Tyr	Asn	Leu	Ala	Ala	Gln	Ser	His	Val	Arg	Val	Ser	Phe	Asp		
			85					90						95			
gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt																	336
Glu	Pro	Val	His	Thr	Gly	Asp	Thr	Thr	Gly	Met	Gly	Ser	Ile	Arg	Leu		
			100					105					110				
ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct																	384
Leu	Glu	Ala	Val	Arg	Leu	Ser	Arg	Val	Asp	Cys	Arg	Phe	Tyr	Gln	Ala		
	115						120					125					
tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg																	432
Ser	Ser	Ser	Glu	Met	Phe		Gly	Ala	Ser	Pro	Pro	Pro	Gln	Asn	Glu	Ser	
	130						135					140					
acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg																	480
Thr	Pro	Phe	Tyr	Pro	Arg	Ser	Pro	Tyr	Gly	Ala	Ala	Lys	Val	Phe	Ser		
145					150					155					160		

tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg	528
Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val	
165 170 175	
aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc	576
Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe	
180 185 190	
gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc	624
Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val	
195 200 205	
caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc	672
Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly	
210 215 220	
tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct	720
Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro	
225 230 235 240	
gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt	768
Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg	
245 250 255	
gag ttc gct caa gct gct ttt gac cat gtc ggg ctc gac tgg caa aag	816
Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys	
260 265 270	
cgc gtc aag ttt gac gac cgc tat ttg cgt ccc acc gag gtc gat tcg	864
Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser	
275 280 285	
cta gta gga gat gcc gac aag gcg gcc cag tca ctc ggc tgg aaa gct	912
Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala	
290 295 300	
tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc	960
Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile	
305 310 315 320	
gcc gcg ttg gag tgc gat gcc aca cca tgg atc gac acg ccg atg ttg	1008
Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu	
325 330 335	
cct ggt tgg ggc aga gta agt tga	1032
Pro Gly Trp Gly Arg Val Ser	
340	
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20 25 30	

Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu  
 50 55 60  
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp  
 65 70 75 80  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95  
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu  
 100 105 110  
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser  
 130 135 140  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser  
 145 150 155 160  
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val  
 195 200 205  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly  
 210 215 220  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro  
 225 230 235 240  
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg  
 245 250 255  
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys  
 260 265 270  
 Arg Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 Leu Val Gly Asp Ala Asp Lys Ala Ala Gln Ser Leu Gly Trp Lys Ala  
 290 295 300  
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile  
 305 310 315 320  
 Ala Ala Leu Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu  
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 Pro Gly Trp Gly Arg Val Ser  
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 ctc gcc gag cta cta ctg agc aag gga tac gag gtt cac ggg ctc gtt 96  
 Leu Ala Glu Leu Leu Ser Lys Gly Tyr Glu Val His Gly Leu Val  
 20 25 30  
 cgt cga gct tcg acg ttt aac acg tcg cgg atc gat cac ctc tac gtt 144  
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 gac cca cac caa ccg ggc gcg cgc ttg ttc ttg cac tat gca gac ctc 192  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu  
 50 55 60  
 act gac ggc acc cgg ttg gtg acc ctg ctc agc agt atc gac ccg gat 240  
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp  
 65 70 75 80  
 gag gtc tac aac ctc gca gcg cag tcc cat gtg cgc gtc agc ttt gac 288  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95  
 gag cca gtg cat acc gga gac acc acc ggc atg gga tcg atc cga ctt 336  
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu  
 100 105 110  
 ctg gaa gca gtc cgc ctt tct cgg gtg gac tgc cgg ttc tat cag gct 384  
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 tcc tcg tcg gag atg ttc ggc gca tct ccg cca ccg cag aac gaa tcg 432  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser  
 130 135 140  
 acg ccg ttc tat ccc cgt tcg cca tac ggc gcg gcc aag gtc ttc tcg 480  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser  
 145 150 155 160  
 tac tgg acg act cgc aac tat cga gag gcg tac gga tta ttc gca gtg 528  
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 aat ggc atc ttg ttc aac cat gag tcc ccc cgg cgc ggc gag act ttc 576  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 gtg acc cga aag atc acg cgt gcc gtg gcg cgc atc cga gct ggc gtc 624  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val  
 195 200 205



caa tcg gag gtc tat atg ggc aac ctc gat gcg atc cgc gac tgg ggc 672  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly  
 210 215 220  
 tac gcg ccc gaa tat gtc gag ggg atg tgg agg atg ttg caa gcg cct 720  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro  
 225 230 235 240  
 gaa cct gat gac tac gtc ctg gcg aca ggg cgt ggt tac acc gta cgt 768  
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg  
 245 250 255  
 gag ttc gct caa gct gct ttt gac cac gtc ggg ctc gac tgg caa aag 816  
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys  
 260 265 270  
 cac gtc aag ttt gac gac cgc tat ttg cgc ccc acc gag gtc gat tcg 864  
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 cta gta gga gat gcc gac agg gcg gcc cag tca ctc ggc tgg aaa gct 912  
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala  
 290 295 300  
 tcg gtt cat act ggt gaa ctc gcg cgc atc atg gtg gac gcg gac atc 960  
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile  
 305 310 315 320  
 gcc gcg tcg gag tgc gat ggc aca cca tgg atc gac acg ccg atg ttg 1008  
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu  
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 cct ggt tgg ggc gga gta agt tga 1032  
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 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Ala Asp Leu  
 50 55 60  
 Thr Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Ser Ile Asp Pro Asp  
 65 70 75 80  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95

Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Ile Arg Leu  
 100 105 110  
 Leu Glu Ala Val Arg Leu Ser Arg Val Asp Cys Arg Phe Tyr Gln Ala  
 115 120 125  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Ser  
 130 135 140  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Phe Ser  
 145 150 155 160  
 Tyr Trp Thr Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Arg Ala Gly Val  
 195 200 205  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Ile Arg Asp Trp Gly  
 210 215 220  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Ala Pro  
 225 230 235 240  
 Glu Pro Asp Asp Tyr Val Leu Ala Thr Gly Arg Gly Tyr Thr Val Arg  
 245 250 255  
 Glu Phe Ala Gln Ala Ala Phe Asp His Val Gly Leu Asp Trp Gln Lys  
 260 265 270  
 His Val Lys Phe Asp Asp Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 Leu Val Gly Asp Ala Asp Arg Ala Ala Gln Ser Leu Gly Trp Lys Ala  
 290 295 300  
 Ser Val His Thr Gly Glu Leu Ala Arg Ile Met Val Asp Ala Asp Ile  
 305 310 315 320  
 Ala Ala Ser Glu Cys Asp Gly Thr Pro Trp Ile Asp Thr Pro Met Leu  
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 Pro Gly Trp Gly Gly Val Ser  
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cag agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc	96
Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro	
20 25 30	
gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt	144
Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg	
35 40 45	
aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act ggc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc ggc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	

gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat 768  
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp 255  
 245 250

ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc 816  
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser 270  
 260 265

gag atc gca gac atg gtc gct aca gcg gtg ggc tac atc ggc gaa aca 864  
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr 285  
 275 280

cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912  
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp 300  
 290 295

gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960  
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys 320  
 305 310 315

gac ggc atc gat gca acg gtg tgc tgg tac cgc aca aat gcc gat gcc 1008  
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala 335  
 325 330

gtg agg agg taa 1020  
 Val Arg Arg

<210> 14  
 <211> 339  
 <212> PRT  
 <213> Mycobacterium

<400> 14  
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Gln Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro 30  
 20 25

Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg 45  
 35 40

Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp 60  
 50 55

Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu 80  
 65 70 75

Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile 95  
 85 90

Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg 110  
 100 105

Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg 125  
 115 120

Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln 140  
 130 135

Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn  
 145 150 155 160  
 Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala  
 165 170 175  
 Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn  
 180 185 190  
 Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu  
 195 200 205  
 Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu  
 210 215 220  
 Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His  
 225 230 235 240  
 Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp  
 245 250 255  
 Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser  
 260 265 270  
 Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr  
 275 280 285  
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300  
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320  
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335  
 Val Arg Arg

<210> 15  
 <211> 1020  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(1017)

<400> 15  
 gtg cga tgg cac acc atg gat cga cac gcc gat gtt gcc tgg ttg ggg 48  
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly  
 1 5 10 15  
 cgg agt aag ttg acg act aca cct ggg cct ctg gac cgc gca acg ccc 96  
 Arg Ser Lys Leu Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro  
 20 25 30  
 gtg tat atc gcc ggt cat cgg ggg ctg gtc ggc tca gcg ctc gta cgt 144  
 Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg  
 35 40 45

aga ttt gag gcc gag ggg ttc acc aat ctc att gtg cga tca cgc gat	192
Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp	
50 55 60	
gag att gat ctg acg gac cga gcc gca acg ttt gat ttt gtg tct gag	240
Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu	
65 70 75 80	
aca aga cca cag gtg atc atc gat gcg gcc gca cgg gtc ggc ggc atc	288
Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile	
85 90 95	
atg gcg aat aac acc tat ccc gcg gac ttc ttg tcc gaa aac ctc cga	336
Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg	
100 105 110	
atc cag acc aat ttg ctc gac gca gct gtc gcc gtg cgt gtg ccg cgg	384
Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg	
115 120 125	
ctc ctt ttc ctc ggt tcg tca tgc atc tac ccg aag tac gct ccg caa	432
Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln	
130 135 140	
cct atc cac gag agt gct tta ttg act gcc cct ttg gag ccc acc aac	480
Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn	
145 150 155 160	
gac gcg tat gcg atc gcc aag atc gcc ggt atc ctg caa gtt cag gcg	528
Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala	
165 170 175	
gtt agg cgc caa tat ggg ctg gcg tgg atc tct gcg atg ccg act aac	576
Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn	
180 185 190	
ctc tac gga ccc gcc gac aac ttc tcc ccg tcc ggg tcg cat ctc ttg	624
Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu	
195 200 205	
ccg gcg ctc atc cgt cga tat gag gaa gcc aaa gct ggt ggt gca gaa	672
Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu	
210 215 220	
gag gtg acg aat tgg ggg acc ggt act ccg cgg cgc gaa ctt ctg cat	720
Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His	
225 230 235 240	
gtc gac gat ctg gcg agc gca tgc ctg ttc ctt ttg gaa cat ttc gat	768
Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp	
245 250 255	
ggt ccg aac cac gtc aac gtg ggc acc ggc gtc gat cac agc att agc	816
Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser	
260 265 270	
gag atc gca gac atg gtc gct acg gcg gtg ggc tac atc ggc gaa aca	864
Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr	
275 280 285	

cgt tgg gat cca act aaa ccc gat gga acc ccg cgc aaa cta ttg gac 912  
 Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300

gtc tcc gcg cta cgc gag ttg ggt tgg cgc ccg cga atc gca ctg aaa 960  
 Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320

gac ggc atc gat gca acg gtg tgg tac cgc aca aat gcc gat gcc 1008  
 Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335

gtg agg agg taa 1020  
 Val Arg Arg

<210> 16  
 <211> 339  
 <212> PRT  
 <213> Mycobacterium

<400> 16  
 Val Arg Trp His Thr Met Asp Arg His Ala Asp Val Ala Trp Leu Gly  
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Arg Ser Lys Leu Thr Thr Thr Pro Gly Pro Leu Asp Arg Ala Thr Pro  
 20 25 30

Val Tyr Ile Ala Gly His Arg Gly Leu Val Gly Ser Ala Leu Val Arg  
 35 40 45

Arg Phe Glu Ala Glu Gly Phe Thr Asn Leu Ile Val Arg Ser Arg Asp  
 50 55 60

Glu Ile Asp Leu Thr Asp Arg Ala Ala Thr Phe Asp Phe Val Ser Glu  
 65 70 75 80

Thr Arg Pro Gln Val Ile Ile Asp Ala Ala Ala Arg Val Gly Gly Ile  
 85 90 95

Met Ala Asn Asn Thr Tyr Pro Ala Asp Phe Leu Ser Glu Asn Leu Arg  
 100 105 110

Ile Gln Thr Asn Leu Leu Asp Ala Ala Val Ala Val Arg Val Pro Arg  
 115 120 125

Leu Leu Phe Leu Gly Ser Ser Cys Ile Tyr Pro Lys Tyr Ala Pro Gln  
 130 135 140

Pro Ile His Glu Ser Ala Leu Leu Thr Gly Pro Leu Glu Pro Thr Asn  
 145 150 155 160

Asp Ala Tyr Ala Ile Ala Lys Ile Ala Gly Ile Leu Gln Val Gln Ala  
 165 170 175

Val Arg Arg Gln Tyr Gly Leu Ala Trp Ile Ser Ala Met Pro Thr Asn  
 180 185 190

Leu Tyr Gly Pro Gly Asp Asn Phe Ser Pro Ser Gly Ser His Leu Leu  
 195 200 205

Pro Ala Leu Ile Arg Arg Tyr Glu Glu Ala Lys Ala Gly Gly Ala Glu  
 210 215 220

Glu Val Thr Asn Trp Gly Thr Gly Thr Pro Arg Arg Glu Leu Leu His  
 225 230 235 240

Val Asp Asp Leu Ala Ser Ala Cys Leu Phe Leu Leu Glu His Phe Asp  
 245 250 255

Gly Pro Asn His Val Asn Val Gly Thr Gly Val Asp His Ser Ile Ser  
 260 265 270

Glu Ile Ala Asp Met Val Ala Thr Ala Val Gly Tyr Ile Gly Glu Thr  
 275 280 285

Arg Trp Asp Pro Thr Lys Pro Asp Gly Thr Pro Arg Lys Leu Leu Asp  
 290 295 300

Val Ser Ala Leu Arg Glu Leu Gly Trp Arg Pro Arg Ile Ala Leu Lys  
 305 310 315 320

Asp Gly Ile Asp Ala Thr Val Ser Trp Tyr Arg Thr Asn Ala Asp Ala  
 325 330 335

Val Arg Arg

<210> 17  
 <211> 723  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(720)

<400> 17  
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 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr  
 1 5 10 15

gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96  
 Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
 20 25 30

aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144  
 Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
 35 40 45

cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192  
 Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
 50 55 60

tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc aag tcg 240  
 Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser  
 65 70 75 80

gca tcg gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288  
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
 85 90 95



gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336  
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
 100 105 110  
 tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384  
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
 115 120 125  
 aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tcg gtt 432  
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
 130 135 140  
 gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480  
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
 145 150 155 160  
 gta cag ggt ttc gag aag cag gtt atc acg ggc agt aag tca acg ctt 528  
 Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu  
 165 170 175  
 aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576  
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
 180 185 190  
 tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624  
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
 195 200 205  
 cta ggt ttc aga ctg acg ggt ttg ttg ccc ggc ttt acg gat ccg cgc 672  
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
 210 215 220  
 aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720  
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
 225 230 235 240  
 tga 723

<210> 18  
 <211> 240  
 <212> PRT  
 <213> Mycobacterium

<400> 18  
 Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr  
 1 5 10 15  
 Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
 20 25 30  
 Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
 35 40 45  
 Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
 50 55 60  
 Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Lys Ser  
 65 70 75 80

Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
85 90 95

Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
100 105 110

Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
115 120 125

Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
130 135 140

Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
145 150 155 160

Val Gln Gly Phe Glu Lys Gln Val Ile Thr Gly Ser Lys Ser Thr Leu  
165 170 175

Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
180 185 190

Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
195 200 205

Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
210 215 220

Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
225 230 235 240

<210> 19  
<211> 723  
<212> DNA  
<213> Mycobacterium

<220>  
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<222> (1)..(720)

<400> 19  
atg gat ttt ttg cgc aac gcc ggc ttg atg gct cgt aac gtt agc acc 48  
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1 5 10 15

gag atg ctg cgc cac ttc gaa cga aag cgc cta tta gta aac caa ttc 96  
Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
20 25 30

aaa gca tac gga gtc aac gtt gtt att gat gtc ggt gct aac tcc ggc 144  
Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
35 40 45

cag ttc ggt agc gct ttg cgt cgt gca gga ttc aag agc cgt atc gtt 192  
Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
50 55 60

tcc ttt gaa cct ctt tcg ggg cca ttt gcg caa cta acg cgc gag tcg 240  
Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser  
65 70 75 80

gca tgc gat cca cta tgg gag tgt cac cag tat gcc cta ggc gac gcc 288  
Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
85 90 95

gat gag acg att acc atc aat gtg gca ggc aat gcg ggg gca agt agt 336  
Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
100 105 110

tcc gtg ctg ccg atg ctt aaa agt cat caa gat gcc ttt cct ccc gcg 384  
Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
115 120 125

aat tat att ggc acc gaa gac gtt gca ata cac cgc ctt gat tgc gtt 432  
Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
130 135 140

gca tca gaa ttt ctg aac cct acc gat gtt act ttc ctg aag atc gac 480  
Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
145 150 155 160

gta cag ggt ttc gag aag cag gtt atc gcg ggc agt aag tca acg ctt 528  
Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu  
165 170 175

aac gaa agc tgc gtc ggc atg caa ctc gaa ctt tct ttt att ccg ttg 576  
Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
180 185 190

tac gaa ggt gac atg ctg att cat gaa gcg ctt gaa ctt gtc tat tcc 624  
Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
195 200 205

cta ggt ttc aga ctg acg ggt ttg ttg ccc gga ttt acg gat ccg cgc 672  
Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
210 215 220

aat ggt cga atg ctt caa gct gac ggc att ttc ttc cgt ggg gac gat 720  
Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
225 230 235 240

tga 723

<210> 20  
<211> 240  
<212> PRT  
<213> Mycobacterium

<400> 20  
Met Asp Phe Leu Arg Asn Ala Gly Leu Met Ala Arg Asn Val Ser Thr  
1 5 10 15

Glu Met Leu Arg His Phe Glu Arg Lys Arg Leu Leu Val Asn Gln Phe  
20 25 30

Lys Ala Tyr Gly Val Asn Val Val Ile Asp Val Gly Ala Asn Ser Gly  
35 40 45

Gln Phe Gly Ser Ala Leu Arg Arg Ala Gly Phe Lys Ser Arg Ile Val  
50 55 60

Ser Phe Glu Pro Leu Ser Gly Pro Phe Ala Gln Leu Thr Arg Glu Ser  
 65 70 75 80  
 Ala Ser Asp Pro Leu Trp Glu Cys His Gln Tyr Ala Leu Gly Asp Ala  
 85 90 95  
 Asp Glu Thr Ile Thr Ile Asn Val Ala Gly Asn Ala Gly Ala Ser Ser  
 100 105 110  
 Ser Val Leu Pro Met Leu Lys Ser His Gln Asp Ala Phe Pro Pro Ala  
 115 120 125  
 Asn Tyr Ile Gly Thr Glu Asp Val Ala Ile His Arg Leu Asp Ser Val  
 130 135 140  
 Ala Ser Glu Phe Leu Asn Pro Thr Asp Val Thr Phe Leu Lys Ile Asp  
 145 150 155 160  
 Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Ser Lys Ser Thr Leu  
 165 170 175  
 Asn Glu Ser Cys Val Gly Met Gln Leu Glu Leu Ser Phe Ile Pro Leu  
 180 185 190  
 Tyr Glu Gly Asp Met Leu Ile His Glu Ala Leu Glu Leu Val Tyr Ser  
 195 200 205  
 Leu Gly Phe Arg Leu Thr Gly Leu Leu Pro Gly Phe Thr Asp Pro Arg  
 210 215 220  
 Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg Gly Asp Asp  
 225 230 235 240

<210> 21  
 <211> 801  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(798)

<400> 21  
 atg act gcg cca gtg ttc tcg ata att atc cct acc ttc aat gca gcg 48  
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala  
 1 5 10 15  
 gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg 96  
 Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg  
 20 25 30  
 gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc 144  
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu  
 35 40 45  
 gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt 192  
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val  
 50 55 60

cac agc ggg ccc gat gat ggc cgc tac gac gcc atg aac cgc ggc gtc 240  
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val  
 65 70 75 80

ggc gtg gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc 288  
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr  
 85 90 95

ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac 336  
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp  
 100 105 110

cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg 384  
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr  
 115 120 125

aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag 432  
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu  
 130 135 140

acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac 480  
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp  
 145 150 155 160

ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac 528  
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp  
 165 170 175

ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg 576  
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met  
 180 185 190

gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg 624  
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg  
 195 200 205

cag ggg act gat aaa gag ttc aga aaa ccg ctg cca atg tac ttc tgg 672  
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp  
 210 215 220

gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac 720  
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp  
 225 230 235 240

aag gag aat cgc cgt ctg gcc ttg cgt acg ccg ttg ata agg gtt aag 768  
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys  
 245 250 255

gcc gtc tcc aaa gaa cga agc gca gaa ccg tag 801  
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro  
 260 265

<210> 22  
 <211> 266  
 <212> PRT  
 <213> Mycobacterium

<400> 22  
 Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala  
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Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg  
 20 25 30  
 Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu  
 35 40 45  
 Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val  
 50 55 60  
 His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val  
 65 70 75 80  
 Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr  
 85 90 95  
 Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp  
 100 105 110  
 His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr  
 115 120 125  
 Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu  
 130 135 140  
 Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp  
 145 150 155 160  
 Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp  
 165 170 175  
 Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met  
 180 185 190  
 Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg  
 195 200 205  
 Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp  
 210 215 220  
 Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp  
 225 230 235 240  
 Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys  
 245 250 255  
 Ala Val Ser Lys Glu Arg Ser Ala Glu Pro  
 260 265

<210> 23  
 <211> 801  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(798)

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1 5 10 15	
gtg acg ctg caa gcc tgc ctc gga agc atc gtc ggg cag acc tac cgg	96
Val Thr Leu Gln Ala Cys Leu Gly Ser Ile Val Gly Gln Thr Tyr Arg	
20 25 30	
gaa gtg gaa gtg gtc ctt gtc gac ggc ggt tcg acc gat cgg acc ctc	144
Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu	
35 40 45	
gac atc gcg aac agt ttc cgc ccg gaa ctc ggc tcg cga ctg gtc gtt	192
Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val	
50 55 60	
cac agc ggg ccc gat gat ggc ccc tac gac gcc atg aac cgc ggc gtc	240
His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val	
65 70 75 80	
ggc gta gcc aca ggc gaa tgg gta ctt ttt tta ggc gcc gac gac acc	288
Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr	
85 90 95	
ctc tac gaa cca acc acg ttg gcc cag gta gcc gct ttt ctc ggc gac	336
Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp	
100 105 110	
cat gcg gca agc cat ctt gtc tat ggc gat gtt gtg atg cgt tcg acg	384
His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr	
115 120 125	
aaa agc cgg cat gcc gga cct ttc gac ctc gac cgc ctc cta ttt gag	432
Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu	
130 135 140	
acg aat ttg tgc cac caa tcg atc ttt tac cgc cgt gag ctt ttc gac	480
Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp	
145 150 155 160	
ggc atc ggc cct tac aac ctg cgc tac cga gtc tgg gcg gac tgg gac	528
Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp	
165 170 175	
ttc aat att cgc tgc ttc tcc aac ccg gcg ctg att acc cgc tac atg	576
Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met	
180 185 190	
gac gtc gtg att tcc gaa tac aac gac atg acc ggc ttc agc atg agg	624
Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg	
195 200 205	
cag ggg act gat aaa gag ttc aga aaa ccg ctg cca atg tac ttc tgg	672
Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp	
210 215 220	
gtt gca ggg tgg gag act tgc agg cgc atg ctg gcg ttt ttg aaa gac	720
Val Ala Gly Trp Glu Thr Cys Arg Arg Met Leu Ala Phe Leu Lys Asp	
225 230 235 240	

aag gag aat cgc cgt ctg gcc ttg cgt acg cgg ttg ata agg gtt aag 768  
Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys  
245 250 255

gcc gtc tcc aaa gaa cga agc gca gaa ccg tag 801  
Ala Val Ser Lys Glu Arg Ser Ala Glu Pro  
260 265

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<210> 24
<211> 266
<212> PRT
<213> Mycobacterium
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<400> 24
Met Thr Ala Pro Val Phe Ser Ile Ile Ile Pro Thr Phe Asn Ala Ala
  1             5             10             15

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20 25 30

Glu Val Glu Val Val Leu Val Asp Gly Gly Ser Thr Asp Arg Thr Leu  
35 40 45

Asp Ile Ala Asn Ser Phe Arg Pro Glu Leu Gly Ser Arg Leu Val Val  
50 55 60

His Ser Gly Pro Asp Asp Gly Pro Tyr Asp Ala Met Asn Arg Gly Val  
65 70 75 80

Gly Val Ala Thr Gly Glu Trp Val Leu Phe Leu Gly Ala Asp Asp Thr  
85 90 95

Leu Tyr Glu Pro Thr Thr Leu Ala Gln Val Ala Ala Phe Leu Gly Asp  
100 105 110

His Ala Ala Ser His Leu Val Tyr Gly Asp Val Val Met Arg Ser Thr  
115 120 125

Lys Ser Arg His Ala Gly Pro Phe Asp Leu Asp Arg Leu Leu Phe Glu  
130 135 140

Thr Asn Leu Cys His Gln Ser Ile Phe Tyr Arg Arg Glu Leu Phe Asp  
145 150 155 160

Gly Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Trp Ala Asp Trp Asp  
165 170 175

Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Ile Thr Arg Tyr Met  
180 185 190

Asp Val Val Ile Ser Glu Tyr Asn Asp Met Thr Gly Phe Ser Met Arg  
195 200 205

Gln Gly Thr Asp Lys Glu Phe Arg Lys Arg Leu Pro Met Tyr Phe Trp  
210 215 220

Val	Ala	Gly	Trp	Glu	Thr	Cys	Arg	Arg	Met	Leu	Ala	Phe	Leu	Lys	Asp
225					230					235					240



Lys Glu Asn Arg Arg Leu Ala Leu Arg Thr Arg Leu Ile Arg Val Lys  
 245 250 255

Ala Val Ser Lys Glu Arg Ser Ala Glu Pro  
 260 265

<210> 25  
 <211> 867  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(864)

<400> 25  
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 Val Ala Ser Arg Ser Pro His Ser Ala Ala Gly Gly Trp Leu Ile Leu  
 1 5 10 15  
 ggc ggc tcc ctt ctt gtg gtc ggc gtg gcg cat ccg gta gga ctc gcc 96  
 Gly Gly Ser Leu Leu Val Val Gly Val Ala His Pro Val Gly Leu Ala  
 20 25 30  
 gga ggt gac gac gat gct ggc gtg gtg cag cag ccg atc gag gat gct 144  
 Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala  
 35 40 45  
 ggc ggc ggt ggt gtg ctc ggg cag gaa tcg ccc cca ttg ttc gaa ggg 192  
 Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly  
 50 55 60  
 cca atg cga ggc gat ggc cag gga gcg gcg ctc gta gcc ggc agc cac 240  
 Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His  
 65 70 75 80  
 gag ccg gaa caa cag ttg agt ccc ggt gtc gtc gag ccg ggc gaa gcc 288  
 Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala  
 85 90 95  
 gat ctc gtc caa gat gac cag atc cgc gcg gag cag ggt gtc gat gat 336  
 Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp  
 100 105 110  
 ctt gcc gac ggt gtt gtc ggc cag gcc gcg gta gag gac ctc gat cag 384  
 Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln  
 115 120 125  
 gtc ggc ggc ggt gaa gta gcg gac ttt gaa tcc ggc gtg gac ggc agc 432  
 Val Gly Gly Gly Glu Val Ala Asp Phe Glu Ser Gly Val Asp Gly Ser  
 130 135 140  
 gtg ccc gca gcc gat gag cag gtg act ttt gcc cgt acc agg tgg gcc 480  
 Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala  
 145 150 155 160  
 aat gac cgc cag gtt ctg ttg tgc ccg aat cca ttc cag gct cga cag 528  
 Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln  
 165 170 175

gta gtc gaa cgt ggc tgc ggt gat cga cga tcc ggt gac gtc gaa ccc 576  
 Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro  
 180 185 190

gtc gag ggt ctt ggt gac cgg gaa ggc tgc ggc ctt gag acg gtt ggc 624  
 Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly  
 195 200 205

ggt gtt gga ggc atc gcg ggc agc gat ctc ggc ctc aac caa cgt ccg 672  
 Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro  
 210 215 220

cag gat ctc ctc cgg tgt cca gcg ttg cgt ctt ggc gac ttg caa cac 720  
 Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His  
 225 230 235 240

ctc ggc ggc gtt gcg gcg cac cgt ggc cag ctt caa ccg ccg cag cgc 768  
 Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg  
 245 250 255

cgc gtc aag gtc agc agc cag cgg tgc cgc cga gga cgg tgc cac cgg 816  
 Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg  
 260 265 270

ctt ggc agc ggt ggt cat gag gcc gtc ccg tcg gtg gtg ttg atc ttg 864  
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 275 280 285

tag 867

<210> 26  
 <211> 288  
 <212> PRT  
 <213> Mycobacterium

<400> 26  
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 20 25 30

Gly Gly Asp Asp Asp Ala Gly Val Val Gln Gln Pro Ile Glu Asp Ala  
 35 40 45

Gly Gly Gly Gly Val Leu Gly Gln Glu Ser Pro Pro Leu Phe Glu Gly  
 50 55 60

Pro Met Arg Gly Asp Gly Gln Gly Ala Ala Leu Val Ala Gly Ser His  
 65 70 75 80

Glu Pro Glu Gln Gln Leu Ser Pro Gly Val Val Glu Arg Gly Glu Ala  
 85 90 95

Asp Leu Val Gln Asp Asp Gln Ile Arg Ala Glu Gln Gly Val Asp Asp  
 100 105 110

Leu Ala Asp Gly Val Val Gly Gln Ala Ala Val Glu Asp Leu Asp Gln  
 115 120 125

Val Gly Gly Gly Glu Val Ala Asp Phe Glu Ser Gly Val Asp Gly Ser  
 130 135 140

Val Pro Ala Ala Asp Glu Gln Val Thr Phe Ala Arg Thr Arg Trp Ala  
 145 150 155 160

Asn Asp Arg Gln Val Leu Leu Cys Pro Asn Pro Phe Gln Ala Arg Gln  
 165 170 175

Val Val Glu Arg Gly Cys Gly Asp Arg Arg Ser Gly Asp Val Glu Pro  
 180 185 190

Val Glu Gly Leu Gly Asp Arg Glu Gly Cys Gly Leu Glu Thr Val Gly  
 195 200 205

Gly Val Gly Gly Ile Ala Gly Ser Asp Leu Gly Leu Asn Gln Arg Pro  
 210 215 220

Gln Asp Leu Leu Arg Cys Pro Ala Leu Arg Leu Gly Asp Leu Gln His  
 225 230 235 240

Leu Gly Gly Val Ala Ala His Arg Gly Gln Leu Gln Pro Pro Gln Arg  
 245 250 255

Arg Val Lys Val Ser Ser Gln Arg Cys Arg Arg Gly Arg Cys His Arg  
 260 265 270

Leu Gly Ser Gly Gly His Glu Ala Val Pro Ser Val Val Leu Ile Leu  
 275 280 285

<210> 27  
 <211> 1739  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(945)

<400> 27  
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 Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val Val Pro Thr  
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ccg gat tat gtg cga ttc gcg tcc cac tat ggc ttc gtt ccg gac ttc 96  
 Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe  
 20 25 30

tgc cac ggt gcg gat ccg caa tcg aag ggc atc gtg gag aac ctc tgt 144  
 Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys  
 35 40 45

ggc tac gct cag gac gac ctt gcg gtg ccg ctg ctg acc gaa gct gcg 192  
 Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala  
 50 55 60

tta gcc ggt gag cag gtc gac cta cgt gcc ctc aac gcc cag gcg caa 240  
 Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln  
 65 70 75 80

cta tgg tgc gcc gag gtc aat gcc acg gtc cac tcg gag atc tgc gcc	288
Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala	
85 90 95	
gtg ccc aac gat cgc ttg gtt gac gag cgc acc gtc ttg agg gag ctg	336
Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu	
100 105 110	
ccc tcg ctg cgg ccg acg atc ggc tcg ggg tcg gtg cgc cgt aag gtc	384
Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val	
115 120 125	
gac ggc ctc tcg tgc atc cgt tac ggc tca gct cgt tac tcg gtg cct	432
Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro	
130 135 140	
cag cgg ctc gtc ggt gcc acc gtg gcg gtg gtg gtc gat cat ggc gcc	480
Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala	
145 150 155 160	
ctg atc ctg ttg gaa cct gcg acc ggt gtg atc gtg gcc gag cac gag	528
Leu Ile Leu Leu Glu Pro Ala Thr Gly Val Ile Val Ala Glu His Glu	
165 170 175	
ctc gtc agc cca ggt gag gtg tcc atc ctc gat gaa cac tac gac gga	576
Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly	
180 185 190	
ccc aga ccc gca ccc tcg cgt ggt cct cgc ccg aaa acc caa gca gag	624
Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu	
195 200 205	
aaa cga ttc tgc gca ttg gga acc gaa gcg cag cag ttc ctc gtc ggt	672
Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly	
210 215 220	
gct gct gcg atc ggc aac acc cga ctg aaa tcc gaa ctc gac att ctg	720
Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu	
225 230 235 240	
ctc ggc ctt ggc gcc gcc cac ggc gaa cag gct ttg att gac gcg ctg	768
Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu	
245 250 255	
cgc cgg gcg gtt gcg ttt cgc cgg ttc cgc gct gcc gac gtg cgc tcg	816
Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser	
260 265 270	
atc ctg gcc gcc ggc gcc ggc acc cca caa ccc cgc ccc gcc ggc gac	864
Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp	
275 280 285	
gca ctc gtg ctc gat ctg ccc acc gtc gag acc cgc tcg ttg gag gcc	912
Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala	
290 295 300	
tac aag atc aac acc acc gac ggg acg gcc tca tgaccaccgc tgccaagccg	965
Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser	
305 310 315	
gtggcaccgt cctcggcggc accgctggt gctgaccttg acgcggcgct gcggcggttg	1025

aagctggcca cgggtgcgccg caacgccgcc gaggtgttgc aagtcgcca gacgcaacgc 1085  
 tggacaccgg aggagatcct gcggacgttg gttgaggccg agatcgctgc ccgcgatgcc 1145  
 tccaacaccg ccaaccgtct caaggccgca gccttcccgg tcaccaagac cctcgacggg 1205  
 ttcgacgtca ccggatcgtc gatcaccgca gccacgttcg actacctgtc gagcctggaa 1265  
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 ctgctcatcg gctgcgggca cgctgccgtc cacgccgat tcaaagtcg ctacttcacc 1385  
 gccgccgacc tgatcgaggt cctctaccgc ggcttgccg acaacaccgt cggcaagatc 1445  
 atcgacaccc tgctccgctc ggatctggtc atcttgacg agatcggctt cggccgctc 1505  
 gacgacaccg ggactcaact gttgttcgg ctcgtggctg ccggctacga gcgccgctcc 1565  
 ctggccatcg cctcgcattg gcccttcgaa caatgggggc gattctgtcc cgagcacacc 1625  
 accgccgcca gcctcctcga tcggctgctg caccacgcca gcctcgtct cacctccggc 1685  
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<210> 28

<211> 315

<212> PRT

<213> Mycobacterium

<400> 28

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 1 5 10 15

Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val Pro Asp Phe  
 20 25 30

Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu Asn Leu Cys  
 35 40 45

Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr Glu Ala Ala  
 50 55 60

Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala Gln Ala Gln  
 65 70 75 80

Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu Ile Cys Ala  
 85 90 95

Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu Arg Glu Leu  
 100 105 110

Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg Arg Lys Val  
 115 120 125

Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr Ser Val Pro  
 130 135 140

Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp His Gly Ala  
 145 150 155 160

Leu Ile Leu Leu Glu Pro<sup>\*</sup> Ala Thr Gly Val Ile Val Ala Glu His Glu  
 165 170 175  
 Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His Tyr Asp Gly  
 180 185 190  
 Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr Gln Ala Glu  
 195 200 205  
 Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe Leu Val Gly  
 210 215 220  
 Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu Asp Ile Leu  
 225 230 235 240  
 Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile Asp Ala Leu  
 245 250 255  
 Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp Val Arg Ser  
 260 265 270  
 Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro Ala Gly Asp  
 275 280 285  
 Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser Leu Glu Ala  
 290 295 300  
 Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser  
 305 310 315

<210> 29

<211> 264

<212> PRT

<213> Mycobacterium

<220>

<221> DOMAIN

<222> (1)..(264)

<223> amino acid sequence is encoded by nucleotides  
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<400> 29

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 20 25 30  
 Arg Arg Asn Ala Ala Glu Val Leu Gln Val Ala Lys Thr Gln Arg Trp  
 35 40 45  
 Thr Pro Glu Glu Ile Leu Arg Thr Leu Val Glu Ala Glu Ile Ala Ala  
 50 55 60  
 Arg Asp Ala Ser Asn Thr Ala Asn Arg Leu Lys Ala Ala Ala Phe Pro  
 65 70 75 80  
 Val Thr Lys Thr Leu Asp Gly Phe Asp Val Thr Gly Ser Ser Ile Thr  
 85 90 95

Ala Ala Thr Phe Asp Tyr Leu Ser Ser Leu Glu Trp Ile Arg Ala Gln  
100 105 110

Gln Asn Leu Ala Val Ile Gly Pro Pro Gly Thr Gly Lys Ser His Leu  
115 120 125

Leu Ile Gly Cys Gly His Ala Ala Val His Ala Gly Phe Lys Val Arg  
130 135 140

Tyr Phe Thr Ala Ala Asp Leu Ile Glu Val Leu Tyr Arg Gly Leu Ala  
145 150 155 160

Asp Asn Thr Val Gly Lys Ile Ile Asp Thr Leu Leu Arg Ala Asp Leu  
165 170 175

Val Ile Leu Asp Glu Ile Gly Phe Ala Pro Leu Asp Asp Thr Gly Thr  
180 185 190

Gln Leu Leu Phe Arg Leu Val Ala Ala Gly Tyr Glu Arg Arg Ser Leu  
195 200 205

Ala Ile Ala Ser His Trp Pro Phe Glu Gln Trp Gly Arg Phe Leu Pro  
210 215 220

Glu His Thr Thr Ala Ala Ser Ile Leu Asp Arg Leu Leu His His Ala  
225 230 235 240

Ser Ile Val Val Thr Ser Gly Glu Ser Tyr Arg Met Arg His Ala Asp  
245 250 255

His Lys Lys Gly Ala Ala Lys Asn  
260

<210> 30  
<211> 789  
<212> DNA  
<213> Mycobacterium

<220>  
<221> CDS  
<222> (1)..(786)

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Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp  
1 5 10 15

ctc gac ggg ttg cag cgc acg gtg aaa agt gtg cgg gcg caa cgc tac 96  
Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr  
20 25 30

cgg gga cgc atc gag cac atc gta atc gac ggt ggc agc ggc gac gac 144  
Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp  
35 40 45

gtg gtg gca tac ctg tcc ggg tgt gaa cca gcc ttc gcg tat tgg cag 192  
Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln  
50 55 60

tcc gag ccc gac ggc ggg. cgg tac gac gcg atg aac cag ggc atc gcg	240
Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala	
65 70 75 80	
cac gca tcg ggt gat ctg ttg tgg ttc ttg cac tcc gcc gat cgt ttt	288
His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe	
85 90 95	
tcc ggg ccc gac gtg gta gcc cag gcc gtg gag gcg cta tcc ggc aag	336
Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys	
100 105 110	
gga ccg gtg tcc gaa ttg tgg ggc ttc ggg atg gat cgt ctc gtc ggg	384
Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly	
115 120 125	
ctc gat cgg gtg cgc ggc ccg ata cct ttc agc ctg cgc aaa ttc ctg	432
Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu	
130 135 140	
gcc ggc aag cag gtt gtt ccg cat caa gca tcg ttc ttc gga tca tcg	480
Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser	
145 150 155 160	
ctg gtg gcc aag atc ggt ggc tac gac ctt gat ttc ggg atc gcc gcc	528
Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala	
165 170 175	
gac cag gaa ttc ata ttg ccg gcc gcg ctg gta tgc gag ccg gtc acg	576
Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr	
180 185 190	
att ccg tgt gtg ctg tgc gag ttc gac acc acg ggc gtc ggc tcg cac	624
Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His	
195 200 205	
ccg gaa cca agc gcg gtc ttc ggt gat ctg cgc cgc atg ggc gac ctt	672
Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu	
210 215 220	
cat cgc cgc tac ccg ttc ggg gga agg cga ata tca cat gcc tac cta	720
His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu	
225 230 235 240	
cgc ggc ccg gag ttc tac gcc tac aac agt cga ttc tgg gaa aac gtc	768
Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val	
245 250 255	
ttc acg cga atg tcg aaa tag	789
Phe Thr Arg Met Ser Lys	
260	

<210> 31  
 <211> 262  
 <212> PRT  
 <213> Mycobacterium

<400> 31  
 Met Thr Ser Ala Pro Thr Val Ser Val Ile Thr Ile Ser Phe Asn Asp  
 1 5 10 15



Leu Asp Gly Leu Gln Arg Thr Val Lys Ser Val Arg Ala Gln Arg Tyr  
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 Arg Gly Arg Ile Glu His Ile Val Ile Asp Gly Gly Ser Gly Asp Asp  
                   35                  40                  45  
 Val Val Ala Tyr Leu Ser Gly Cys Glu Pro Gly Phe Ala Tyr Trp Gln  
                   50                  55                  60  
 Ser Glu Pro Asp Gly Gly Arg Tyr Asp Ala Met Asn Gln Gly Ile Ala  
                   65                  70                  75                  80  
 His Ala Ser Gly Asp Leu Leu Trp Phe Leu His Ser Ala Asp Arg Phe  
                   85                  90                  95  
 Ser Gly Pro Asp Val Val Ala Gln Ala Val Glu Ala Leu Ser Gly Lys  
                   100                  105                  110  
 Gly Pro Val Ser Glu Leu Trp Gly Phe Gly Met Asp Arg Leu Val Gly  
                   115                  120                  125  
 Leu Asp Arg Val Arg Gly Pro Ile Pro Phe Ser Leu Arg Lys Phe Leu  
                   130                  135                  140  
 Ala Gly Lys Gln Val Val Pro His Gln Ala Ser Phe Phe Gly Ser Ser  
                   145                  150                  155                  160  
 Leu Val Ala Lys Ile Gly Gly Tyr Asp Leu Asp Phe Gly Ile Ala Ala  
                   165                  170                  175  
 Asp Gln Glu Phe Ile Leu Arg Ala Ala Leu Val Cys Glu Pro Val Thr  
                   180                  185                  190  
 Ile Arg Cys Val Leu Cys Glu Phe Asp Thr Thr Gly Val Gly Ser His  
                   195                  200                  205  
 Arg Glu Pro Ser Ala Val Phe Gly Asp Leu Arg Arg Met Gly Asp Leu  
                   210                  215                  220  
 His Arg Arg Tyr Pro Phe Gly Gly Arg Arg Ile Ser His Ala Tyr Leu  
                   225                  230                  235                  240  
 Arg Gly Arg Glu Phe Tyr Ala Tyr Asn Ser Arg Phe Trp Glu Asn Val  
                   245                  250                  255  
 Phe Thr Arg Met Ser Lys  
                   260

<210> 32  
 <211> 1023  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(1020)

<400> 32  
 gtg aag cga gcg ctc atc acc gga atc acc ggc cag gac ggc tcg tat 48  
 Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr  
 1 5 10 15  
  
 ctc gcc gaa ctg ctg ctg gcc aag ggg tat gag gtt cac ggg ctc atc 96  
 Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile  
 20 25 30  
  
 cgg cgc gct tcg acg ttc aac acc tcg cgg atc gat cac ctc tac gtc 144  
 Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45  
  
 gac ccg cac caa ccg ggc gcg cgg ctg ttt ctg cac tat ggt gac ctg 192  
 Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu  
 50 55 60  
  
 atc gac gga acc cgg ttg gtg acc ctg ctg agc acc atc gaa ccc gac 240  
 Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp  
 65 70 75 80  
  
 gag gtg tac aac ctg gcg gcg cag tca cac gtg cgg gtg agc ttc gac 288  
 Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95  
  
 gaa ccc gtg cac acc ggt gac acc acc ggc atg gga tcc atg cga ctg 336  
 Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu  
 100 105 110  
  
 ctg gaa gcc gtt cgg ctc tct cgg gtg cac tgc cgc ttc tat cag gcg 384  
 Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala  
 115 120 125  
  
 tcc tcg tcg gag atg ttc ggc gcc tcg ccg cca ccg cag aac gag ctg 432  
 Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu  
 130 135 140  
  
 acg ccg ttc tac ccg cgg tca ccg tat ggc gcc gcc aag gtc tat tcg 480  
 Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser  
 145 150 155 160  
  
 tac tgg gcg acc cgc aat tat cgc gaa gcg tac gga ttg ttc gcc gtc 528  
 Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
  
 aac ggc atc ttg ttc aat cac gaa tca ccg cgg cgc ggt gag acg ttc 576  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
  
 gtg acc cga aag atc acc agg gcc gtg gca cgc atc aag gcc ggt atc 624  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile  
 195 200 205  
  
 cag tcc gag gtc tat atg ggc aat ctg gat gcg gtc cgc gac tgg ggg 672  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly  
 210 215 220  
  
 tac gcg ccc gaa tac gtc gaa ggc atg tgg cgg atg ctg cag acc gac 720  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp  
 225 230 235 240

gag ccc gac gac ttc gtt<sup>\*</sup> ttg geg acc ggg cgc ggt ttc acc gtg cgt 768  
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg  
 245 250 255

gag ttc gcg cgg gcc gcg ttc gag cat gcc ggt ttg gac tgg cag cag 816  
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln  
 260 265 270

tac gtg aaa ttc gac caa cgc tat ctg cgg ccc acc gag gtg gat tcg 864  
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285

ctg atc ggc gac gcg acc aag gct gcc gaa ttg ctg ggc tgg agg gct 912  
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala  
 290 295 300

tcg gtg cac act gac gag ttg gct cgg atc atg gtc gac gcg gac atg 960  
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met  
 305 310 315 320

gcg gcg ctg gag tgc gaa ggc aag ccg tgg atc gac aag ccg atg atc 1008  
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile  
 325 330 335

gcc ggc cgg aca tga 1023  
 Ala Gly Arg Thr  
 340

<210> 33  
 <211> 340  
 <212> PRT  
 <213> Mycobacterium

<400> 33

Met Lys Arg Ala Leu Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr  
 1 5 10 15

Leu Ala Glu Leu Leu Leu Ala Lys Gly Tyr Glu Val His Gly Leu Ile  
 20 25 30

Arg Arg Ala Ser Thr Phe Asn Thr Ser Arg Ile Asp His Leu Tyr Val  
 35 40 45

Asp Pro His Gln Pro Gly Ala Arg Leu Phe Leu His Tyr Gly Asp Leu  
 50 55 60

Ile Asp Gly Thr Arg Leu Val Thr Leu Leu Ser Thr Ile Glu Pro Asp  
 65 70 75 80

Glu Val Tyr Asn Leu Ala Ala Gln Ser His Val Arg Val Ser Phe Asp  
 85 90 95

Glu Pro Val His Thr Gly Asp Thr Thr Gly Met Gly Ser Met Arg Leu  
 100 105 110

Leu Glu Ala Val Arg Leu Ser Arg Val His Cys Arg Phe Tyr Gln Ala  
 115 120 125

Ser Ser Ser Glu Met Phe Gly Ala Ser Pro Pro Pro Gln Asn Glu Leu  
 130 135 140

Thr Pro Phe Tyr Pro Arg Ser Pro Tyr Gly Ala Ala Lys Val Tyr Ser  
 145 150 155 160  
 Tyr Trp Ala Thr Arg Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Val  
 165 170 175  
 Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Thr Phe  
 180 185 190  
 Val Thr Arg Lys Ile Thr Arg Ala Val Ala Arg Ile Lys Ala Gly Ile  
 195 200 205  
 Gln Ser Glu Val Tyr Met Gly Asn Leu Asp Ala Val Arg Asp Trp Gly  
 210 215 220  
 Tyr Ala Pro Glu Tyr Val Glu Gly Met Trp Arg Met Leu Gln Thr Asp  
 225 230 235 240  
 Glu Pro Asp Asp Phe Val Leu Ala Thr Gly Arg Gly Phe Thr Val Arg  
 245 250 255  
 Glu Phe Ala Arg Ala Ala Phe Glu His Ala Gly Leu Asp Trp Gln Gln  
 260 265 270  
 Tyr Val Lys Phe Asp Gln Arg Tyr Leu Arg Pro Thr Glu Val Asp Ser  
 275 280 285  
 Leu Ile Gly Asp Ala Thr Lys Ala Ala Glu Leu Leu Gly Trp Arg Ala  
 290 295 300  
 Ser Val His Thr Asp Glu Leu Ala Arg Ile Met Val Asp Ala Asp Met  
 305 310 315 320  
 Ala Ala Leu Glu Cys Glu Gly Lys Pro Trp Ile Asp Lys Pro Met Ile  
 325 330 335  
 Ala Gly Arg Thr  
 340

<210> 34  
 <211> 732  
 <212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(729)

<400> 34  
 atg agg ctg gcc cgt cgc gct cgg aac atc ttg cgt cgc aac ggc atc 48  
 Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile  
 1 5 10 15  
 gag gtg tcg cgc tac ttt gcc gaa ctg gac tgg gaa cgc aat ttc ttg 96  
 Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu  
 20 25 30

cgc caa ctg caa tcg cat.cgg gtc agt gcc gtg ctc gat gtc ggg gcc	144
Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala	
35 40 45	
aat tcg ggg cag tac gcc agg ggt ctg cgc ggc gcg ggc ttc gcg ggc	192
Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly	
50 55 60	
cgc atc gtc tcg ttc gag ccg ctg ccc ggg ccc ttt gcc gtc ttg cag	240
Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln	
65 70 75 80	
cgc agc gcc tcc acg gac ccg ttg tgg gaa tgc cgg cgc tgt gcg ctg	288
Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu	
85 90 95	
ggc gat gtc gat gga acc atc tcg atc aac gtc gcc ggc aac gag ggc	336
Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly	
100 105 110	
gcc agc agt tcc gtc ttg ccg atg ttg aaa cga cat cag gac gcc ttt	384
Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe	
115 120 125	
cca cca gcc aac tac gtg ggc gcc caa cgg gtg ccg ata cat cga ctc	432
Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu	
130 135 140	
gat tcc gtg gct gca gac gtt ctg cgg ccc aac gat att gcg ttc ttg	480
Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu	
145 150 155 160	
aag atc gac gtt caa gga ttc gag aag cag gtg atc gcg ggt ggc gat	528
Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp	
165 170 175	
tca acg gtg cac gac cga tgc gtc ggc atg cag ctc gag ctg tct ttc	576
Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe	
180 185 190	
cag ccg ttg tac gag ggt ggc atg ctc atc cgc gag gcg ctc gat ctc	624
Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu	
195 200 205	
gtg gat tcg ttg ggc ttt acg ctc tcg gga ttg caa ccc ggt ttc acc	672
Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr	
210 215 220	
gac ccc cgc aac ggt cga atg ctg cag gcc gat ggc atc ttc ttc cgg	720
Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg	
225 230 235 240	
ggc agc gat tga	732
Gly Ser Asp	

&lt;210&gt; 35

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium

&lt;400&gt; 35

Met Arg Leu Ala Arg Arg Ala Arg Asn Ile Leu Arg Arg Asn Gly Ile  
 1 5 10 15

Glu Val Ser Arg Tyr Phe Ala Glu Leu Asp Trp Glu Arg Asn Phe Leu  
 20 25 30

Arg Gln Leu Gln Ser His Arg Val Ser Ala Val Leu Asp Val Gly Ala  
 35 40 45

Asn Ser Gly Gln Tyr Ala Arg Gly Leu Arg Gly Ala Gly Phe Ala Gly  
 50 55 60

Arg Ile Val Ser Phe Glu Pro Leu Pro Gly Pro Phe Ala Val Leu Gln  
 65 70 75 80

Arg Ser Ala Ser Thr Asp Pro Leu Trp Glu Cys Arg Arg Cys Ala Leu  
 85 90 95

Gly Asp Val Asp Gly Thr Ile Ser Ile Asn Val Ala Gly Asn Glu Gly  
 100 105 110

Ala Ser Ser Ser Val Leu Pro Met Leu Lys Arg His Gln Asp Ala Phe  
 115 120 125

Pro Pro Ala Asn Tyr Val Gly Ala Gln Arg Val Pro Ile His Arg Leu  
 130 135 140

Asp Ser Val Ala Ala Asp Val Leu Arg Pro Asn Asp Ile Ala Phe Leu  
 145 150 155 160

Lys Ile Asp Val Gln Gly Phe Glu Lys Gln Val Ile Ala Gly Gly Asp  
 165 170 175

Ser Thr Val His Asp Arg Cys Val Gly Met Gln Leu Glu Leu Ser Phe  
 180 185 190

Gln Pro Leu Tyr Glu Gly Gly Met Leu Ile Arg Glu Ala Leu Asp Leu  
 195 200 205

Val Asp Ser Leu Gly Phe Thr Leu Ser Gly Leu Gln Pro Gly Phe Thr  
 210 215 220

Asp Pro Arg Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg  
 225 230 235 240

Gly Ser Asp

&lt;210&gt; 36

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Mycobacterium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(729)

<400> 36  
 gtg aaa tcg ttg aaa ctg gct cgt ttc atc gcg cgt agc gcc gcc ttc 48  
 Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe  
 1 5 10 15

gag gtt tcg cgc cgc tat tct gag cga gac ctg aag cac cag ttt gtg 96  
 Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val  
 20 25 30

aag caa ctc aaa tcg cgt cgg gta gat gtc gtt ttc gat gtc gcc gcc 144  
 Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala  
 35 40 45

aac tca gga caa tac gcc gcc gcc ctc cgc cga gca gca tat aag gcc 192  
 Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly  
 50 55 60

cgc att gtc tcg ttc gaa ccg cta tcc gga ccg ttt acg atc ttg gaa 240  
 Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu  
 65 70 75 80

agc aaa gcg tca acg gat cca ctt tgg gat tgc cgg cag cat gcg ttg 288  
 Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu  
 85 90 95

ggc gat tct gat gga acg gtt acg atc aat atc gca gga aac gcc ggt 336  
 Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly  
 100 105 110

cag agc agt tcc gtc ttg ccc atg ctg aaa agt cat cag aac gct ttt 384  
 Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe  
 115 120 125

ccc ccg gca aac tat gtc ggt acc caa gag gcg tcc ata cat cga ctt 432  
 Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu  
 130 135 140

gat tcc gtg gcg cca gaa ttt cta ggc atg aac ggt gtc gct ttt ctc 480  
 Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu  
 145 150 155 160

aag gtc gac gtt caa gcc ttt gaa aag cag gtg ctc gcc ggg gcc aaa 528  
 Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys  
 165 170 175

tca acc ata gat gac cat tgc gtc gcc atg caa ctc gaa ctg tcc ttc 576  
 Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe  
 180 185 190

ctg ccg ttg tac gaa ggt gcc atg ctc att cct gaa gcc ctc gat ctc 624  
 Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu  
 195 200 205

gtg tat tcc ttg gcc ttc acg ttg acg gga ttg ctg cct tgt ttc att 672  
 Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile  
 210 215 220

gat gca aat aat ggt cga atg ttg cag gcc gac gcc atc ttt ttc cgc 720  
 Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg  
 225 230 235 240

gag gac gat tga  
Glu Asp Asp

<210> 37  
<211> 243  
<212> PRT  
<213> Mycobacterium

<400> 37  
Met Lys Ser Leu Lys Leu Ala Arg Phe Ile Ala Arg Ser Ala Ala Phe  
1 5 10 15  
Glu Val Ser Arg Arg Tyr Ser Glu Arg Asp Leu Lys His Gln Phe Val  
20 25 30  
Lys Gln Leu Lys Ser Arg Arg Val Asp Val Val Phe Asp Val Gly Ala  
35 40 45  
Asn Ser Gly Gln Tyr Ala Ala Gly Leu Arg Arg Ala Ala Tyr Lys Gly  
50 55 60  
Arg Ile Val Ser Phe Glu Pro Leu Ser Gly Pro Phe Thr Ile Leu Glu  
65 70 75 80  
Ser Lys Ala Ser Thr Asp Pro Leu Trp Asp Cys Arg Gln His Ala Leu  
85 90 95  
Gly Asp Ser Asp Gly Thr Val Thr Ile Asn Ile Ala Gly Asn Ala Gly  
100 105 110  
Gln Ser Ser Ser Val Leu Pro Met Leu Lys Ser His Gln Asn Ala Phe  
115 120 125  
Pro Pro Ala Asn Tyr Val Gly Thr Gln Glu Ala Ser Ile His Arg Leu  
130 135 140  
Asp Ser Val Ala Pro Glu Phe Leu Gly Met Asn Gly Val Ala Phe Leu  
145 150 155 160  
Lys Val Asp Val Gln Gly Phe Glu Lys Gln Val Leu Ala Gly Gly Lys  
165 170 175  
Ser Thr Ile Asp Asp His Cys Val Gly Met Gln Leu Glu Leu Ser Phe  
180 185 190  
Leu Pro Leu Tyr Glu Gly Gly Met Leu Ile Pro Glu Ala Leu Asp Leu  
195 200 205  
Val Tyr Ser Leu Gly Phe Thr Leu Thr Gly Leu Leu Pro Cys Phe Ile  
210 215 220  
Asp Ala Asn Asn Gly Arg Met Leu Gln Ala Asp Gly Ile Phe Phe Arg  
225 230 235 240  
Glu Asp Asp

<210> 38  
<211> 828



<212> DNA  
 <213> Mycobacterium

<220>  
 <221> CDS  
 <222> (1)..(825)

<400> 38

atg gtg cag acg aaa cga tac gcc ggc ttg acc gca gct aac aca aag	48
Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys	
1 5 10 15	
aaa gtc gcc atg gcc gca cca atg ttt tcg atc atc atc ccc acc ttg	96
Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu	
20 25 30	
aac gtg gct gcg gta ttg cct gcc tgc ctc gac agc atc gcc cgt cag	144
Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln	
35 40 45	
acc tgc ggt gac ttc gag ctg gta ctg gtc gac ggc ggc tcg acg gac	192
Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp	
50 55 60	
gaa acc ctc gac atc gcc aac att ttc gcc ccc aac ctc ggc gag cgg	240
Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg	
65 70 75 80	
ttg atc att cat cgc gac acc gac cag ggc gtc tac gac gcc atg aac	288
Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn	
85 90 95	
cgc ggc gtg gac ctg gcc acc gga acg tgg ttg ctc ttt ctg ggc gcg	336
Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala	
100 105 110	
gac gac agc ctg tac gag gct gac acc ctg gcg cgg gtg gcc gcc ttc	384
Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe	
115 120 125	
att ggc gaa cac gag ccc agc gat ctg gta tat ggc gac gtg atc atg	432
Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met	
130 135 140	
cgc tca acc aat ttc cgc tgg ggt ggc gcc ttc gac ctc gac cgt ctg	480
Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu	
145 150 155 160	
ttg ttc aag cgc aac atc tgc cat cag gcg atc ttc tac cgc cgc gga	528
Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly	
165 170 175	
ctc ttc ggc acc atc ggt ccc tac aac ctc cgc tac cgg gtc ctg gcc	576
Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala	
180 185 190	
gac tgg gac ttc aat att cgc tgc ttt tcc aac cca gcg ctc gtc acc	624
Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr	
195 200 205	

cgc tac atg cac gtg gtc gtt gca agc tac aac gaa ttc ggc ggg ctc 672  
 Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu  
 210 215 220  
 agc aat acg atc gtc gac aag gag ttt ttg aag cgg ctg ccg atg tcc 720  
 Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser  
 225 230 235 240  
 acg aga ctc ggc ata agg ctg gtc ata gtt ctg gtg cgc agg tgg cca 768  
 Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro  
 245 250 255  
 aag gtg atc agc agg gcc atg gta atg cgc acc gtc att tct tgg cgg 816  
 Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg  
 260 265 270  
 cgc cga cgt tag 828  
 Arg Arg  
 275

<210> 39  
 <211> 275  
 <212> PRT  
 <213> Mycobacterium

<400> 39  
 Met Val Gln Thr Lys Arg Tyr Ala Gly Leu Thr Ala Ala Asn Thr Lys  
 1 5 10 15  
 Lys Val Ala Met Ala Ala Pro Met Phe Ser Ile Ile Ile Pro Thr Leu  
 20 25 30  
 Asn Val Ala Ala Val Leu Pro Ala Cys Leu Asp Ser Ile Ala Arg Gln  
 35 40 45  
 Thr Cys Gly Asp Phe Glu Leu Val Leu Val Asp Gly Gly Ser Thr Asp  
 50 55 60  
 Glu Thr Leu Asp Ile Ala Asn Ile Phe Ala Pro Asn Leu Gly Glu Arg  
 65 70 75 80  
 Leu Ile Ile His Arg Asp Thr Asp Gln Gly Val Tyr Asp Ala Met Asn  
 85 90 95  
 Arg Gly Val Asp Leu Ala Thr Gly Thr Trp Leu Leu Phe Leu Gly Ala  
 100 105 110  
 Asp Asp Ser Leu Tyr Glu Ala Asp Thr Leu Ala Arg Val Ala Ala Phe  
 115 120 125  
 Ile Gly Glu His Glu Pro Ser Asp Leu Val Tyr Gly Asp Val Ile Met  
 130 135 140  
 Arg Ser Thr Asn Phe Arg Trp Gly Gly Ala Phe Asp Leu Asp Arg Leu  
 145 150 155 160  
 Leu Phe Lys Arg Asn Ile Cys His Gln Ala Ile Phe Tyr Arg Arg Gly  
 165 170 175

Leu Phe Gly Thr Ile Gly Pro Tyr Asn Leu Arg Tyr Arg Val Leu Ala  
 180 185 190  
 Asp Trp Asp Phe Asn Ile Arg Cys Phe Ser Asn Pro Ala Leu Val Thr  
 195 200 205  
 Arg Tyr Met His Val Val Val Ala Ser Tyr Asn Glu Phe Gly Gly Leu  
 210 215 220  
 Ser Asn Thr Ile Val Asp Lys Glu Phe Leu Lys Arg Leu Pro Met Ser  
 225 230 235 240  
 Thr Arg Leu Gly Ile Arg Leu Val Ile Val Leu Val Arg Arg Trp Pro  
 245 250 255  
 Lys Val Ile Ser Arg Ala Met Val Met Arg Thr Val Ile Ser Trp Arg  
 260 265 270  
 Arg Arg Arg  
 275

<210> 40  
 <211> 24  
 <212> DNA  
 <213> Mycobacterium

<400> 40  
 gatgccgtga ggaggtaaag ctgc

24

<210> 41  
 <211> 24  
 <212> DNA  
 <213> Mycobacterium

<400> 41  
 gatacggctc ttgaatcctg cacg

24